

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run On: February 23, 2001, 10:48:45 ; Search time 15.7 Seconds
(without alignments)
765.504 Million cell updates/sec

Title: US-09-195-368-1
Perfect score: 951
Sequence: 1 MCLSHLENPLSHSRTOGAQ.....VLKNNTYWGIIILLANPOFIS 177

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_66: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	82	8.6	1188	A71621	protein with 5'-3'
2	79.5	8.4	665	T18979	hypothetical prote
3	79.5	8.4	851	T51545	receptor protein k
4	78	8.2	564	S73405	hexosephosphate tr
5	77.5	8.1	352	D82442	probable peptide A
6	77.5	8.1	880	S49627	regulatory protein
7	77	8.1	326	1 VGRDSD	glycoprotein vp7 p
8	77	8.1	326	1 VGRHNN	glycoprotein vp7 p
9	77	8.1	326	1 VGRHUU	glycoprotein vp7 p
10	76.5	8.0	233	S11688	tumor necrosis fac
11	76	8.0	525	E70125	hypothetical prote
12	75.5	7.9	222	T14847	MADS-box protein d
13	75.5	7.9	314	T50811	MHC class I protel
14	75.5	7.9	686	T20898	hypothetical prote
15	75	7.9	129	B35216	FP14 protein - low
16	75	7.9	575	T28230	ORF MSV069 probabl
17	74.5	7.8	233	S22052	tumor necrosis fac
18	74.5	7.8	355	A48976	GTP-binding regula
19	74.5	7.8	465	T41511	probable dolichol
20	74.5	7.8	471	S28476	rflb protein VC024
21	74.5	7.8	543	S68467	CD40 receptor-asso
22	74	7.8	567	T49272	CD40 receptor-asso
23	74	7.8	568	A55649	TNFR-associated pr
24	74	7.8	568	A55960	CD40 receptor-asso
25	73.5	7.7	345	E71858	hypothetical prote
26	73.5	7.7	504	T47446	hypothetical prote
27	73.5	7.7	609	A34358	replication protei
28	73	7.7	166	S12723	interferon gamma p
29	73	7.7	326	1 VGRDSD	glycoprotein vp7 p

glycoprotein vp7 p
neurotoxin type F
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
penicillin-binding
penicillin-binding
probable purine nu
hypothetical prote
sporamin A (clone
ASP-56 protein - p
tumor necrosis fac
Sd protein - fruit
protein with DnaJ
conserved hypothet
intrinsic factor-B

ALIGNMENTS

RESULT 1
A71621
protein with 5'-3' exonuclease domain (Kem-1 family) PFB0205c - malaria parasite (Pla
C:Species: Plasmodium falciparum
C:Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000
C:Accession: A71621
R: Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.
; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H
Science 282, 1126-1132, 1998
A:Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A:Reference number: A71600; MUID:99021743
A:Accession: A71621
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-1188 <GAR>
A:Cross-references: GB:AE001380; GB:AE001362; NID:G3845120; PIDN:AAC71830.1; PID:G384
A:Experimental source: clone 3D7
C:Genetics:
A:Gene: PFB0205C

Query Match 8.6%; Score 82; DB 2; Length 1188;
Best local Similarity 30.4%; Pred. No. 12;
Matches 38; Conservative 11; Mismatches 36; Indels 40; Gaps 9;
Qy 41 FSWLIFIFLQLETAKEPCMAKEG-PLPSKQWASSEPPCV-----NKVSDW----KLEIL 90
Db 7 YMWLVFLFFLE-----LAKGIPCLHKW-VINNFPSCVKIVDRNKLIDWNCIGKLEKA 59
Qy 91 Q-----NGLYLIYGQVAPNANVNDVAPFVRLYKKNKDMITQTLTNKSKION 135
Db 60 KGKHKRNHNGDNGDNGDNNYDNDNNYDNGCEIN-RNIKND--NTYDN-----N 111
Qy 136 VGGTY 140
Db 112 INNTY 116

RESULT 2
T18979
hypothetical protein C06B3.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
C:Accession: T18979
R:Percy, C.
submitted to the EMBL Data Library, July 1996
A:Reference number: Z19056
A:Accession: T18979
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-665 <WIL>
A:Cross-references: EMBL:Z77652; PIDN:CAB01113.1; GSPDB:GN00023; CESP:C06B3.2

A:Experimental source: clone C06B3

C:Genetics:

A:Gene: CESP:C06B3.2

A:Map position: 5

A:Introns: 29/3; 91/1; 139/3; 205/2; 240/1; 296/1; 337/3; 390/1; 419/3; 483/2; 556/2; 58

C:Superfamily: Caenorhabditis elegans hypothetical protein F09B9.1

Query Match 8.4%; Score 79.5; DB 2; Length 665;
Best Local Similarity 21.2%; Pred. No. 10;
Matches 44; Conservative 24; Mismatches 61; Indels 79; Gaps 9;

QY 27 WLPCSVMLLLFLCSFSLWIFLFIQLETAKEPCMAKFGPLPSKWQMASSEPPCCVKNVSDW- 85

Db 7 FLFC-----LLKFVCSHGSLYFGKIES-----PEPFSSFINSHVTPECTKDKMTWI 55

QY 86 -----KLEILONGLYLI--YGQVA--PNANYNDVAPFEVRLYK 119

Db 56 SSIEQFTAASSDCLPFKNCTASILNLDNIYAIQYDAFAKIPAGLLEVSFLVFDGSYQ 115

QY 120 NKDMIOQL-----KSKIONVGGTYELH-----VGDTIDL- 150

Db 116 ECHRISGVKYETNYCVLLVPGRNANCSGSIQNAAGTSVAFRRAYCMPKSCASSDTVDLY 175

QY 151 -----IFNSEHQLVKNNTYWG 166

Db 176 NQLSALPLTACATFCSDRDVDPKDSAFWG 203

RESULT 3

T51545

receptor protein kinase-like protein - Arabidopsis thaliana

N:Alternate names: protein F2K13.50

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000

C:Accession: T51545

R:Sato, S.; Nakamura, Y.; Kaneko, T.; Kato, T.; Asamizu, E.; Kotani, H.; Tabata, S.; Mew

submitted to the Protein Sequence Database, August 2000

A:Reference number: Z25394

A:Accession: T51545

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-851 <SAT>

A:Cross-references: EMBL:AL391141

A:Experimental source: cultivar Columbia; BAC clone F2K13

C:Genetics:

A:Map position: 5

A:Introns: 23/1; 202/2; 371/1; 428/2; 452/2; 476/2; 531/1; 602/3; 645/1; 667/1; 730/2

A:Note: F2K13_50

Query Match 8.4%; Score 79.5; DB 2; Length 851;
Best Local Similarity 22.2%; Pred. No. 14;
Matches 41; Conservative 25; Mismatches 44; Indels 75; Gaps 8;

QY 43 WLIFLFIQLETAKEPCMAKFGPLPSKWQMASSEPPCCVKNV-----SD----- 84

Db 7 YLFFIFAIHYVQ-----AQOGFISLDCGLPSNEPPYIEPVTGLVFSSDADHIPSGISGRI 62

QY 85 -----WKLEILONGLYLI-----YGQVAPNANYNDVAPFE 114

Db 63 QKNLEAVHIKPYLFYRFPDGLRCNYLIDLVLRNRYMIKAVFYVGNV---DGYNDYPSFD 119

QY 115 VRLYXNKDMIOQLTNKSKIONVGGTYE--LHV-----GDTIDLIFNSEHQVL 159

Db 120 LYLGNKVVVRDLECK-----VNGSVEEIIHPPSSNSIQICLVKTGNSLFFISALELRLL 174

QY 160 KNTTY 164

Db 175 RNDTY 179

RESULT 4

S73405

hexosephosphate transport protein uhpT - Mycoplasma pneumoniae (strain ATCC 29342)

N:Alternate names: hypothetical protein h02_Orf5640

C:Species: Mycoplasma pneumoniae

A:Variety: ATCC 29342

C:Date: 26-Feb-1997 #sequence_revision 25-Apr-1997 #text_change 07-Dec-1999

C:Accession: S73405

R:Himmelfreid, R.; Hilbert, H.; Plagens, H.; Pirk, E.; Li, B.C.; Hermann, R.

Nucleic Acids Res. 24, 4420-4449, 1996

A:Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae

A:Reference number: S73327; MUID:97105885

A:Accession: S73405

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-564 <HIM>

A:Cross-references: EMBL:AE000010; GB:U00089; NID:91673729; PIDN:AAB95727.1; PID:g167

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996

C:Genetics:

A:Gene: uhpT

A:Genetic code: SGC3

Query Match 8.2%; Score 78; DB 2; Length 564;
Best Local Similarity 22.9%; Pred. No. 11;
Matches 33; Conservative 22; Mismatches 45; Indels 44; Gaps 8;

QY 17 QGAQRSSWKLWLFCSIVMLL----FLCSFSLWIFLFIQLETAKEPCMAKFGPLPSKWQMA 72

Db 238 QSVQAGCTKYVVFILTAIILIGFGLCVFAW-----FEKQMDPEMPQ---KQTKQEQM 287

QY 73 SSEPPCVNKV-----SDWK-----LEILON-----GLYLIYQVAPNANYNDVAPFEVR 116

Db 288 LGNQPSAGDILKRAWKMKMGYGICLVLVNPLTGGWNILQAVSPASSFN----- 339

QY 117 LYKNKDMIOQLTNKSKIONVGGTY 140

Db 340 ---VKDGVKTL---KPLEGAGGYF 357

RESULT 5

D82442

probable peptide ABC transporter, permease protein VCA0589 [imported] - Vibrio cholerae

C:Species: Vibrio cholerae

C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 15-Sep-2000

C:Accession: D82442

R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.

chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers

l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000

A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A:Reference number: A82035; MUID:20406833

A:Accession: D82442

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-352 <HEI>

A:Cross-references: GB:AE004389; GB:AE003853; NID:98657989; PIDN:AAF96491.1; GSPDB:GN

A:Experimental source: serogroup O1; strain N16961; biotype El Tor

C:Genetics:

A:Gene: VCA0589

A:Map position: 2

Query Match 8.1%; Score 77.5; DB 2; Length 352;
Best Local Similarity 26.3%; Pred. No. 7.3;
Matches 31; Conservative 19; Mismatches 35; Indels 33; Gaps 8;

QY 10 PLSH-----SRTQGAQRSSWKLWLFCSIVMLLFLCSFSLWIFLFIQLETAKEPCMAKFGPLP 66

Db 14 PLTEARWARFANRRGFWLSLWIF----LLLFVVS-----LFAELLANDKPLLIQY---D 60

QY 67 SKWOMASSEPPCCVKNVSDWKLEILONGLYLIYQVAPNANYNDVAPFEVRLYKNDKI 124

Db 61 GAWYM-----PIQVRYSE-----TQFG-----GEFTDADYTD--PYVVSLEERQGI 101

RESULT 6

S49627
regulatory protein ARG2 - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein YML099C
C:Species: Saccharomyces cerevisiae
C>Date: 02-Dec-1994 #sequence_revision 10-Feb-1995 #text_change 24-Sep-1999
C:Accession: S49627; A25064
R:Centiles, S.; Bowman, S.
submitted to the EMBL Data Library, November 1994
A:Reference number: S49627
A:Accession: S49627
A:Molecule type: DNA
A:Residues: 1-880 <GEN>
A:CROSS-references: EMBL:Z46660; NID:g575702; PID:g575703; MIPS:YML099C
R:Mesenguy, F.; Dubois, E.; Descamps, F.
Eur. J. Biochem. 157, 77-81, 1986
A:Title: Nucleotide sequence of the ARG2 regulatory gene and amino acid sequence homology
A:Reference number: A25064; MUID:86220196
A:Accession: A25064
A:Molecule type: DNA
A:Residues: 1-3, 'F', 'S', '128, '130-131, 'L', '132-282, 'V', '284-344, 'V', '346-365, 'Q', '367-548, 'A', '550-551
C:Genetics:
A:Gene: SGD:ARG81; ARG2
A:CROSS-references: MIPS:YML099C; SGD:S0004565
A:Map position: 13L
C:Superfamily: unassigned GAL4-type zinc cluster proteins; GAL4 zinc binuclear cluster
C:Keywords: DNA binding; nucleus
F:16-53/Domain: GAL4 zinc binuclear cluster homology <GAL4>

Query Match 8.1%; Score 77.5; DB 2; Length 880;
Best Local Similarity 22.7%; Pred. No. 22;
Matches 37; Conservative 35; Mismatches 54; Indels 37; Gaps 8;

QY 45 IFIFLQ---ETAKEPCMAK-----FGPLPSKQWOMASSEPPCVNRY-----82
DB 555 IFSPFLKIQDSTALDVKRAKIVLLPSEEDDNYKPLDTSNATSSSEPRVDVQVQGLFRE 614
QY 83 -----SDMK--LEILQNGLYLYGOVAPNAN-----YNDVAPFEVRLYKMKDMITQITNKS 132
DB 615 ALNENDGKIHFVKEPITNVSADSTPSTPTPIFNIA---TESYNNKSDISKLVSKTD 671

QY 133 IONVGYELH-VGDTIDIFNSEHQLKNTYWGIIILANPQ 174
DB 672 -ENIIGTDSLYGLPNSLILLLFSDCVIRVHRNXYNYLTPVPR 713

RESULT 7

VGXRDS
glycoprotein VP7 precursor - human rotavirus A (serotype 2 strain DS1)
N:Alternate names: outer capsid protein VP7
C:Species: human rotavirus A
C>Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 16-Feb-1997
C:Accession: S49627
R:Green, K.Y.; Midthun, K.; Gorziglia, M.; Hoshino, Y.; Kapikian, A.Z.; Chanock, R.M.;
Virology 161, 153-159, 1987
A:Title: Comparison of the amino acid sequences of the major neutralization protein of
A:Reference number: A27620; MUID:88044489
A:Accession: A27620
A:Molecule type: genomic RNA
A:Residues: 1-326 <GRE>
C:Genetics:
A:Map position: segment 9
C:Superfamily: rotavirus glycoprotein VP7
C:Keywords: coat protein; glycoprotein; transmembrane protein
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-326/Product: glycoprotein VP7 #status predicted <GPV>
F:32-48/Region: hydrophobic #status predicted
F:69,146,238/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 8.1%; Score 77; DB 1; Length 326;
Best Local Similarity 22.8%; Pred. No. 7.4;
Matches 42; Conservative 29; Mismatches 59; Indels 54; Gaps 9;

QY 26 LWFCSIVMLLFLC-----SFSWLIFFILOLETAKEPCMAK-----FGPLPSKQWOM 71
DB 10 LTLISILLNYILKTIITMDYIIFRLLIALLISPFVRYTONYGMVLPITGSLDAVYTN 69
QY 72 ASSEPP-----CV-----NKVSDMKLEILQNGLYLYGOVAPNA---NYNDVAPFEV 115
DB 70 STSGEPFLTSLCLYYPAAKNEISDDDEWNTLSQLFLTKGWPIGSVYPKDYNDINTFSV 129
QY 116 --RLYKMKDMIQITNKSQIONVGGTYELHVGDTIDIFNSEHQLKNTYWGIIILANP 173
DB 130 NPQLCYDYNV-----LMRYDNTSELDASELADLIINE-----W-----LCNP 167

QY 174 QFIS 177

DB 168 MDIS 171

RESULT 8

VGXRHN
glycoprotein VP7 precursor - human rotavirus A (serotype 2 strain HN126)
N:Alternate names: outer capsid protein VP7
C:Species: human rotavirus A
C>Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 16-Feb-1997
C:Accession: F27620
R:Green, K.Y.; Midthun, K.; Gorziglia, M.; Hoshino, Y.; Kapikian, A.Z.; Chanock, R.M.;
Virology 161, 153-159, 1987
A:Title: Comparison of the amino acid sequences of the major neutralization protein of
A:Reference number: A27620; MUID:88044489
A:Accession: F27620
A:Molecule type: genomic RNA
A:Residues: 1-326 <GRE>
C:Genetics:
A:Map position: segment 9
C:Superfamily: rotavirus glycoprotein VP7
C:Keywords: coat protein; glycoprotein; transmembrane protein
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-326/Product: glycoprotein VP7 #status predicted <GPV>
F:32-48/Region: hydrophobic #status predicted
F:69,146,238/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 8.1%; Score 77; DB 1; Length 326;
Best Local Similarity 22.8%; Pred. No. 7.4;
Matches 42; Conservative 29; Mismatches 59; Indels 54; Gaps 9;

QY 26 LWFCSIVMLLFLC-----SFSWLIFFILOLETAKEPCMAK-----FGPLPSKQWOM 71
DB 10 LTLISILLNYILKTIITMDYIIFRLLIALLISPFVRYTONYGMVLPITGSLDAVYTN 69
QY 72 ASSEPP-----CV-----NKVSDMKLEILQNGLYLYGOVAPNA---NYNDVAPFEV 115
DB 70 STSGEPFLTSLCLYYPAAKNEISDDDEWNTLSQLFLTKGWPIGSVYPKDYNDINTFSV 129
QY 116 --RLYKMKDMIQITNKSQIONVGGTYELHVGDTIDIFNSEHQLKNTYWGIIILANP 173
DB 130 NPQLCYDYNV-----LMRYDNTSELDASELADLIINE-----W-----LCNP 167

QY 174 QFIS 177

DB 168 MDIS 171

RESULT 9

VGXRHU
glycoprotein VP7 precursor - human rotavirus A
N:Alternate names: outer capsid protein VP7
C:Species: human rotavirus A
C>Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 16-Jul-1999
C:Accession: G27620; A93520; A04134

R.Green, K.Y.; Midthun, K.; Gorziglia, M.; Hoshino, Y.; Kapikian, A.Z.; Chanock, R.M.; Virology 161, 153-159, 1987
 A:Title: Comparison of the amino acid sequences of the major neutralization protein of
 A:Reference number: A27620; MUID:88044489
 A:Accession: G27620
 A:Molecule type: genomic RNA
 A:Residues: 1-326 <GRE>
 A:Experimental source: serotype 2 strain HU5
 R:Dyall-Smith, M.L.; Holmes, I.H. Nucleic Acids Res. 12, 3973-3982, 1984
 A:Title: Sequence homology between human and animal rotavirus serotype-specific glycoprotein
 A:Reference number: A93520; MUID:84221410
 A:Accession: A93520
 A:Molecule type: DNA
 A:Residues: 1-326 <DYA>
 A:Cross-references: GB:X00572; NID:g61680; PIDN:CAA25236.1; PID:g61681
 A:Experimental source: serotype 2 strain Hu/Australia/5/7
 C:Genetics:
 A:Map position: segment 9
 C:Superfamily: rotavirus glycoprotein VP7
 C:Keywords: coat protein; glycoprotein; transmembrane protein
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:24-326/Product: glycoprotein VP7 #status predicted <GPV>
 F:32-48/Region: hydrophobic #status predicted
 F:69,146,238/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 8.1%; Score 77; DB 1; Length 326;
 Best Local Similarity 22.8%; Pred. NO. 7.4;
 Matches 42; Conservative 29; Mismatches 59; Indels 54; Gaps 9;
 QY 26 LWFCSIVMLFLFC-----SFSMLIFLETAKEPCMAK-----EGPLPSKQW 71
 Db 10 LTLISILLNLIKTIWMIIFRELLIALISPVRTQNGYGMVLPITGSLDAVYN 69
 QY 72 ASSEPP-----CV-----NKVSDWKLEILQNGLYLIYQVAPNA---NYNDVAPVEV 115
 Db 70 STSGEPFLSTLCIYAPAAKNEISDEWENTLSOLFETKWPISGVYFKDYNINFSV 129
 QY 116 --RLYKNKDMITLTKSKIONGVGTIELHVGDTIDLIFNSEHOVLKNYWGIIILANP 173
 Db 130 NPQLYCDYNNV-----LMRYDNTSELDASELADILNE-----W-----LCNP 167
 QY 174 QFTS 177
 Db 168 MDIS 171

RESULT 10
 S11688
 tumor necrosis factor alpha precursor - cat
 C:Species: Felis silvestris catus (domestic cat)
 C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 04-Feb-2000
 C:Accession: S11688
 R:McGraw, R.A.; Coffee, B.W.; Otto, C.M.; Drews, R.T.; Rawlings, C.A. Nucleic Acids Res. 18, 5563, 1990
 A:Title: Gene sequence of feline tumor necrosis factor alpha.
 A:Reference number: S11688; MUID:91016860
 A:Accession: S11688
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-233 <MCG>
 A:Cross-references: EMBL:X54000; NID:g1084; PIDN:CAA37948.1; PID:g295777
 C:Genetics:
 A:Introns: 62/3; 78/1; 94/1
 C:Superfamily: tumor necrosis factor
 C:Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein
 F:19,20/Binding site: myristate (Lys) (covalent) #status predicted
 F:81/Binding site: carbohydrate (Ser) (covalent) #status predicted
 F:145-177/Disulfide bonds: #status predicted

Query Match 8.0%; Score 76.5; DB 2; Length 233;

Best Local Similarity 20.2%; Pred. NO. 5.6;
 Matches 50; Conservative 31; Mismatches 54; Indels 113; Gaps 12;
 QY 7 ENMPLSHSRTOGAQRSGSWKWLWLFCSIVMLLFLCSFSWLIF-----IFLOLETAKEPCMAK 61
 Db 15 EALPKKAGGPGSGR-----CLCLSLFSLVAGATTIF-----CLLH 52
 QY 62 FG-----PLPSKQWMA-----SEPPCVN----- 80
 Db 53 FGVIQFQREELPHGLQINPLPOTLRSSSRTPSKPVAHVANPEAGLOLSPRRANAL 112
 QY 81 -----KVSDWKLEILQNGLYLIYQV-----APNANY-----NDVAPFEVRLYKKNKDMIT 126
 Db 113 LANGVELTNDOLKVPDGLYLIYQVLFVGGCPSTHVLTLTHAISRFAYSVQTKNNILSA 172
 QY 127 LTNKSKIQN-----VGGTYELHVGDTID-----LIENSEHOVLKNN 162
 Db 173 I--KSPQRETPEGAPAKPWEPYILGGVQLEKGDRLSTEINLPAYLDFAESGV----- 226
 QY 163 TYWGIILL 170
 Db 227 -YFGIIL 233
 RESULT 11
 E70125
 hypothetical protein BB0205 - Lyme disease spirochete
 C:Species: Borrelia burgdorferi (Lyme disease spirochete)
 C:Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 28-Jul-2000
 C:Accession: E70125
 R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; Wh
 son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vu
 Bowman, C.; Garland, S.; Fujii, C.; Coton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
 Nature 390, 580-586, 1997
 A:Authors: Smith, H.O.; Venter, J.C.
 A:Title: Genomic sequence of a Lyme disease spirochete, Borrelia burgdorferi.
 A:Reference number: A70100; MUID:98065943
 A:Accession: E70125
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Residues: 1-525 <KLE>
 A:Molecule type: DNA
 A:Cross-references: GB:AE001131; GB:AE000783; NID:g2688098; PIDN:AAC66601.1; PID:g268
 A:Experimental source: strain B31
 C:Superfamily: Borrelia burgdorferi hypothetical protein BB0205

Query Match 8.0%; Score 76; DB 2; Length 525;
 Best Local Similarity 23.1%; Pred. NO. 16;
 Matches 37; Conservative 28; Mismatches 53; Indels 42; Gaps 7;
 QY 44 LIFTFLOLETAKE---PCMAKFGPLP-----SKWQMASSEPPPCVKNVSKWKLEI 89
 Db 345 LVRFICIVDYDELVNPFIKESANPLETVKFLIENSGKYWYNSRKEPQTKNKKFDIKM 404
 QY 90 LONGLYLI-----YQOVAP-----NANYNDVAPFEVRL-----YKNKDMI 124
 Db 405 LENLFTILAPFDYQIVDVNKNKNNENLFOAAVLEYKMSIAPNLSINKKNTQYKEEII 464
 QY 125 QLTNKS-KIONVGGTYELHVGDTID--LIENSEHOVLKNN 161
 Db 465 MDLENKEILIKDANGYKKNPLNNVDVFIKNSIPELNKN 504

RESULT 12
 T14847
 MADS-box protein dal2 - Norway spruce
 C:Species: Picea abies (Norway spruce)
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
 C:Accession: T14847
 R:Tandré, K.; Albert, V.A.; Sundas, A.; Engström, P. Plant Mol. Biol. 27, 69-78, 1995
 A:Title: Conifer homologues to genes that control floral development in angiosperms.
 A:Reference number: S51934; MUID:95170009

A:Accession: T14847
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-222 <TAN>
A:Cross-references: EMBL:X79280; NID:g695687; PIDN:CAA55867.1; PID:g695688
A:Experimental source: female cone
C:Genetics:
A:Gene: dal2
C:Superfamily: transcription factor squa; serum response factor DNA-binding domain homol
C:Keywords: DNA binding; transcription regulation
F:2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 7.9%; Score 75.5; DB 2; Length 222;
Best Local Similarity 20.0%; Pred. No. 6.5;
Matches 32; Conservative 32; Mismatches 65; Indels 31; Gaps 5;

QY 15 RTQGAORSSKWLWLFCSIVMLLFCSFWLIFIFLQ-----LETAKEPCM-AKFGPLPS 67
DB 24 RRGLLKAYELSVLCDAEVALIVFSSRGRLYEFANHSVKRTIERYKKTCDVNNHGGVIS 83
QY 68 K-----WOMASSEPCPVKNVSKDWKLEILONGLYLYGOVAPNANVNDVAPFVRLYKNKD 122
DB 84 ENSNQYQCEAGK-----LRQIEILQANRHLMDGLTALNIKELKQLEVRLEKGG 136
QY 123 MIOTLNKSKIONGVGYELHVGDTIDLFNSEHVLKNN 162
DB 137 RVRSKKNEMLLEF-----IDIMORREHILIOEN 164

RESULT 13
I50811
MHC class I protein, alpha 1, alpha 2, alpha 3 and transmembrane domains - coelacanth (f
C:Species: Latimeria chalumnae (coelacanth)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 03-Dec-1999
C:Accession: I50811
R:Betz, U.A.K.; Mayer, W.E.; Klein, J.
Proc. Natl. Acad. Sci. U.S.A. 91, 11065-11069, 1994
A:Title: Major histocompatibility complex class I genes of the coelacanth Latimeria cha
A:Reference number: I50810; MUID:95062206
A:Accession: I50811
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-314 <BET>
A:Cross-references: EMBL:U08034; NID:g549857; PIDN:AAA52346.1; PID:g560544
C:Genetics:
A:Gene: Lach-UB-01
A:Introns: 91/1; 183/1; 276/1
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match 7.9%; Score 75.5; DB 2; Length 314;
Best Local Similarity 34.2%; Pred. No. 9.9;
Matches 26; Conservative 9; Mismatches 26; Indels 15; Gaps 5;

QY 55 KPCMAKFGPLPSKQWASSEPCCVKNVSKDWKLEILONGLYLYGOVAPNANVNDVAP 112
DB 138 KAOIRSKVCPVDEAMDSVFSF-----DWKQECIE-GLKKYLLYGR---ETLERKQVAP 185
QY 113 FEVRLYKNKDMIOQLT 128
DB 186 -EVRYDRPDLERNLT 200

RESULT 14
T20898
hypothetical protein F14F3.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T20898
R:Kershaw, J.
submitted to the EMBL Data Library, June 1995
A:Reference number: Z19343

A:Accession: T20898
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-686 <WLL>
A:Cross-references: EMBL:Z49937; PIDN:CAA90184.1; GSPDB:GN00028; CESP:F14F3.2
A:Experimental source: clone F14F3
C:Genetics:
A:Gene: CESP:F14F3.2
A:Map position: X
A:Introns: 9/1; 49/1; 76/2; 100/2; 151/2; 212/3; 314/3; 380/2; 447/2; 508/2; 622/3; 6

Query Match 7.9%; Score 75.5; DB 2; Length 686;
Best Local Similarity 22.6%; Pred. No. 25;
Matches 40; Conservative 26; Mismatches 64; Indels 47; Gaps 6;

QY 11 LSHSRTOGAORSSKWLWLFCSIVMLLFCSFWLIFIFLQLETAKEPCMAGFGPLPSKWQ 70
DB 319 MSAARNRQRK-----LAKFTPIQFTILLIDLIKDKRRITGDNPA--- 359
QY 71 MASSEPP-CVNKVSQWKLLEILONGLYLYGOV-----PNANYN----- 108
DB 360 -PVSEPPKNRKSNDTPLRMKKSEYADYDEVAGISCSPIGIVPNQANTLDESSRVW 418
QY 109 -DVAPFVRLYKNKDMIOQLTNKSKIONGVGYELHVGDTIDLFNSEHVLKNNKY 164
DB 419 DELLEMKERLSTETMTVVTLK-----QNEELTKLVHSLQAQNNINLSLITFRDLY 471

RESULT 15
B35216
F14 protein - fowlpox virus (strain PP-1)
C:Species: fowlpox virus
C:Date: 23-Aug-1991 #sequence_revision 23-Aug-1991 #text_change 24-Nov-1999
C:Accession: B35216
R:Tartaglia, J.; Winslow, J.; Goebel, S.; Johnson, G.P.; Taylor, J.; Paoletti, E.
J. Gen. Virol. 71, 1517-1524, 1990
A:Title: Nucleotide sequence analysis of a 10.5 kbp HindIII fragment of fowlpox virus
A:Reference number: A35216; MUID:90324937
A:Accession: B35216
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-129 <VAR>
A:Cross-references: GB:X17202; NID:g61222; PIDN:CAA35065.1; PID:g61225
C:Superfamily: fowlpox virus protein F14

Query Match 7.9%; Score 75; DB 2; Length 129;
Best Local Similarity 28.8%; Pred. No. 3.8;
Matches 23; Conservative 14; Mismatches 37; Indels 6; Gaps 3;

QY 31 STVMLFLCSFWLIFIFLQLETAKEPCMAGFGPLPSKWQ---ASSEPPCVNKVSKWKL 87
DB 6 SIYVLTGVGSCFYNPFI-LTYECRDDCCNGRYGVPAPKRWLNCTKTGCGCPD--SGYLL 62
QY 88 EILQGLYLYGOVAPNANY 107
DB 63 TTSENKTYCITGNETDKGY 82

Search completed: February 23, 2001, 10:49:52
Job time: 67 sec

